

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 31, 2002, 15:19:17 ; Search time 30.12 seconds  
(without alignments)  
62.691 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Seq. source: 1 LOTPOPLQVMEPOGD 17  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

A.GeneSeq.032802.\*  
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22: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	17	22	AA872247
2	89	100.0	17	22	AA872501
3	89	100.0	17	22	AA872533
4	89	100.0	17	22	AA859310
5	89	100.0	17	22	AA859341
6	56	62.9	11	22	AAE07185
7	56	62.9	12	22	AAE07195
8	46	51.7	693	19	AA80722
9	46	51.7	693	22	AA807640
10	46	51.7	693	22	AA801093
11	45	50.6	83	22	AB829372

12	45	50.6	83	22	AB834546	Peptide #2052 enco
13	45	50.6	83	22	AB819955	Protein #1954 enco
14	45	50.6	83	22	AA855332	Human brain expres
15	45	50.6	83	22	AA867726	Human bone marrow
16	45	50.6	83	22	AA815539	Peptide #1973 enco
17	45	50.6	83	22	AA828029	Peptide #2066 enco
18	45	50.6	83	22	AA803288	Peptide #1970 enco
19	45	50.6	667	19	AA848760	BOP1 protein. Mus
20	44	49.4	133	20	AA807279	Bovine synuclein.
21	44	49.4	134	20	AA807278	Human beta-synucle
22	43	48.3	417	22	AA808962	Human nGPCR58 #1.
23	43	48.3	419	22	AA808975	Human nGPCR58 #3.
24	43	48.3	468	21	AA871295	Human orphan G pro
25	43	48.3	468	21	AA802829	Human G-protein co
26	43	48.3	470	21	AA894267	Human G-protein co
27	43	48.3	470	21	AA894268	Human G-protein co
28	43	48.3	470	22	AA810175	Human G-protein co
29	43	48.3	470	22	AA804567	Human G-protein co
30	43	48.3	470	22	AA846838	Human nGPCR58 #2.
31	43	48.3	505	22	AA808974	HSV-2 strain SB5 C
32	43	48.3	552	19	AA872233	HSV-2 strain SB5 C
33	43	48.3	725	19	AA872234	HSV-2 strain SB5 C
34	43	48.3	754	19	AA872235	HSV-2 strain SB5 C
35	43	48.3	772	19	AA872236	HSV-2 strain SB5 C
36	43	48.3	772	19	AA872237	HSV-2 strain SB5 C
37	43	48.3	794	19	AA872238	HSV-2 strain SB5 C
38	43	48.3	799	19	AA872239	HSV-2 strain SB5 C
39	43	48.3	819	19	AA872240	HSV-2 strain SB5 C
40	43	48.3	826	19	AA872241	HSV-2 strain SB5 C
41	42	47.2	92	22	AA890144	C glutamicum prote
42	42	47.2	95	22	AA890144	Human polypeptide
43	42	47.2	348	22	AA842050	Rat GABA-A recepto
44	42	47.2	557	21	AA853701	Novel human diagno
45	42	47.2	773	22	AB815668	

## ALIGNMENTS

RESULT 1

AA872247 standard; peptide; 17 AA.

AA872247:

14-MAY-2001 (first entry)

Colostriin derived cytokine inducing peptide SEQ ID 2.

Colostriin; Immune response; cytokine; blood cell proliferation;  
central nervous system disorder; neurological disorder; mental disorder;  
dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
neurosis; infection.

Synthetic.

WO200111937-A2.

22-FEB-2001.

17-AUG-2000; 2000WO-US22818.

17-AUG-1999; 99US-0149311.

(TEXA) UNIV TEXAS SYSTEM.  
(REG- ) REGEN THERAPEUTICS PLC.

Stanton GJ, Hughes TK, Bologh I, Georgiades J,

WPI; 2001-202804/20.

Inducing a cytokine and modulating an immune response, useful for  
treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological  
 XX regulator -  
 PS Claim 1: Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqplqymepgqd 17

RESULT 2  
 AAB72501  
 ID AAB72501 standard; Peptide; 17 AA.  
 XX  
 AC AAB72501;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #2.  
 XX  
 KM Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000MO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanion GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI: 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqplqymepgqd 17

RESULT 3  
 AAB72533  
 ID AAB72533 standard; Peptide; 17 AA.  
 XX  
 AC AAB72533;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #2.  
 XX  
 KM Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KM colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000MO-US22774.  
 XX  
 PR 17-AUG-1999; 99US-0149633.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI: 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqplqymepgqd 17

RESULT 4  
 AAB59310  
 ID AAB59310 standard; Peptide; 17 AA.  
 XX  
 AC AAB59310;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-1.  
 XX  
 KM Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;



Example 2; Page 8; 40pp; English.

PS Claim 3; Pages 312-314; 333pp; English



derived from mRNA of human breast, and then measuring the label

[illegible]

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;  
 Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 OY 1 LGTPPPLQVMEPQ 15  
 ||||| : ||  
 21 lqkppllaslaaspq 35

Standard; Protein; 83 AA.

49955;

DT 23-JAN-2002 (first entry)

DE Protein #1954 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT hearts -

XX Claim 15; SEQ ID NO 21725; 530pp; English.

PS The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABA21535-ABA41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosing diseases of the

CC human heart and vascular system e.g. cardiovascular disease,

CC hypertension, cardiac arrhythmias and congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pcl\_sequences.

XX Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;

Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LGTPPPLQVMEPQ 15  
 ||||| : ||  
 Db 21 lqkppllaslaaspq 35

RESULT 14

AA55332  
 ID AAM55332 standard; Protein; 83 AA.

AC AAM55332;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27437.

XX Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains -

XX Example 4; SEQ ID NO: 27437; 650pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is a protein encoded by one of

CC the probes of the invention.

XX Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;  
 Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LGTPPPLQVMEPQ 15  
 ||||| : ||  
 Db 21 lqkppllaslaaspq 35

RESULT 15

AA67729  
 ID AAM67729 standard; Protein; 83 AA.

AC AAM67729;

XX

DT

06-NOV-2001 (first entry)

XX

DE

Human bone marrow expressed probe encoded protein SEQ ID NO: 28035.

XX

KW

Human; bone marrow expressed exon; gene expression analysis; probe;

XX

microarray; cancer; leukemia; lymphoma; myeloma.

XX

Homo sapiens.

XX

PN

WO200157276-A2.

XX

PD

09-AUG-2001.

XX

PF

30-JAN-2001; 2001WO-US00668.

XX

PR

04-FEB-2000; 2000US-0180312.

XX

26-MAY-2000; 2000US-0207456.

PR

30-JUN-2000; 2000US-0608408.

XX

03-AUG-2000; 2000US-0632366.

PR

21-SEP-2000; 2000US-0234687.

XX

27-SEP-2000; 2000US-0236359.

PR

04-OCT-2000; 2000GB-0024263.

XX

PA

(MOLE-) MOLECULAR DYNAMICS INC.

XX

PI

Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR

WPI; 2001-488900/53.

XX

PT

Human genome-derived single exon nucleic acid probes useful for

XX

analyzing gene expression in human bone marrow -

XX

PS

Example 4; SEQ ID NO: 28035; 658bp + Sequence Listing; English.

XX

CC

The present invention provides a number of single exon nucleic acid

XX

probes which are derived from genomic sequences expressed in the human

XX

bone marrow. They can be used to measure gene expression in bone marrow

XX

samples, which may enable the improved diagnosis and treatment of cancers

XX

such as lymphoma, leukemia and myeloma. The present sequence is a

XX

sequence encoded by one of the probes of the invention.

83 AA;

RESULT

ID

AB019955

XX

50.6%; Score 45; DB 22; Length 83;

XX

60.0%; Pred. NO. 7.1;

XX

Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX

VMMEPQ 15

XX

11

XX

31aspq 35

Completed: July 31, 2002, 15:23:25  
 Time: 248 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:21:17 ; Search time 12.85 seconds

(without alignments)  
32.314 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89

Sequence: 1 LQTPQPLQVMEPQGD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
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- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	41	46.1	343	3	US-08-858-003-32
3	41	46.1	343	3	US-09-078-166-32
4	41	46.1	343	4	US-08-997-467-32
5	41	46.1	428	4	US-09-347-833-6
6	40.5	45.5	369	2	US-08-596-291-4
7	40.5	45.5	369	5	US-09-100-804-4
8	40.5	45.5	369	5	PCT-US94-09943-4
9	40.5	45.5	671	4	US-09-121-321-16
10	40.5	45.5	671	4	US-08-933-803A-16
11	38.5	43.3	179	4	US-08-858-207A-456
12	38	42.7	1276	4	US-09-297-937C-13
13	37	41.6	328	4	US-09-225-244-2
14	37	41.6	328	4	US-09-417-242-2
15	36.5	41.0	2441	1	US-08-194-468-2
16	36.5	41.0	2441	1	US-08-961-739-2
17	36	40.4	210	1	US-08-078-090-2
18	36	40.4	213	4	US-09-131-028A-2
19	36	40.4	213	4	US-09-131-028A-2
20	36	40.4	366	3	US-08-945-056-8
21	36	40.4	390	1	US-08-335-583C-2
22	36	40.4	615	3	US-08-860-091A-4
23	36	40.4	618	3	US-08-834-306-65
24	36	40.4	618	4	US-08-993-674A-65
25	36	40.4	1106	1	US-08-180-195-2
26	36	40.4	1106	1	US-08-168-917-2
27	36	40.4	1106	1	US-08-477-329-2

## ALIGNMENTS

28	36	40.4	1106	2	US-08-475-458-2	Sequence 2, App11
29	36	40.4	1106	2	US-08-460-510-2	Sequence 2, App11
30	36	40.4	1106	2	US-08-460-490-2	Sequence 2, App11
31	36	40.4	1106	3	US-08-980-400-2	Sequence 2, App11
32	36	40.4	1106	3	US-08-462-728-4	Sequence 4, App11
33	36	40.4	1106	4	US-09-583-459A-2	Sequence 2, App11
34	36	40.4	1106	4	US-09-583-210-2	Sequence 2, App11
35	36	40.4	1106	4	US-09-583-449A-2	Sequence 2, App11
36	36	40.4	1106	5	PCT-US82-00720-2	Sequence 2, App11
37	36	40.4	1106	5	PCT-US92-00862-2	Sequence 2, App11
38	36	40.4	4545	2	US-08-804-227C-14	Sequence 14, App11
39	36	40.4	4550	2	US-08-804-227C-8	Sequence 8, App11
40	36	40.4	4550	2	US-08-804-198-2	Sequence 2, App11
41	35	39.3	357	1	US-08-638-911A-37	Sequence 37, App11
42	35	39.3	439	3	US-08-993-359-24	Sequence 24, App11
43	35	39.3	439	3	US-09-221-654-2	Sequence 2, App11
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45	35	39.3	504	1	US-07-932-915-2	Sequence 2, App11

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RESULT 1
US-08-718-661-2
; Sequence 2, Application US/08718661
; Patent No. 5876972
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Nucleic acid molecules coding for mammalian
; TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,661
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 667 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-661-2

Query Match      50.6%; Score 45; DB 2; Length 667;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY      1 LQTPQPLQVMEPQ 15
DB      543 LPVPQPLPQMPQ 557

RESULT 2
US-08-858-003-32
; Sequence 32, Application US/08858003
; Patent No. 6060234
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassl, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaolan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
; NUMBER OF SEQUENCES: 34

```

1 CORRESPONDENCE ADDRESS:  
2 ADDRESSEE: Abbott Laboratories  
3 STREET: 100 Abbott Park Rd.  
4 CITY: Abbott Park  
5 STATE: Illinois  
6 COUNTRY: USA  
7 ZIP: 60064-3500  
8 COMPUTER READABLE FORM:  
9 MEDIUM TYPE: Diskette  
10 COMPUTER: IBM Compatible  
11 OPERATING SYSTEM: DOS  
12 SOFTWARE: FASTSEQ Version 2.0  
13 CURRENT APPLICATION DATA:  
14 APPLICATION NUMBER: US/08/858, 003  
15 FILING DATE: 16-MAY-1979  
16 CLASSIFICATION: 435  
17 PRIOR APPLICATION DATA:  
18 APPLICATION NUMBER:  
19 FILING DATE:  
20 ATTORNEY/AGENT INFORMATION:  
21 NAME: Dianne Casuto  
22 REGISTRATION NUMBER: P-40,943  
23 REFERENCE/DOCKET NUMBER: 4952.US.P2  
24 TELECOMMUNICATION INFORMATION:  
25 TELEPHONE: (847)-938-3137  
26 TELEFAX: (847)-938-2623  
27 TELEX:  
28 INFORMATION FOR SEQ ID NO: 32:  
29 SEQUENCE CHARACTERISTICS:  
30 LENGTH: 343 amino acids  
31 TYPE: amino acid  
32 STRANDEDNESS: single  
33 TOPOLOGY: linear  
34 MOLECULE TYPE: No. 6060234e  
35 US-08-858-003-32

Query Match 46.1%; Score 41; DB 3; Length 343;  
Best Local Similarity 46.7%; Pred. No. 41;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPLQVMEPQG 16  
1 1:11 1: 1:1  
DB 42 QLPRKLVLEPQG 56

RESULT 3  
US-09-078-166-32  
Sequence 32, Application US/09078166  
Patent No. 6063561  
GENERAL INFORMATION:  
APPLICANT: Katz, Leonard  
APPLICANT: Stassl, Diane L.  
APPLICANT: Summers Jr., Richard G.  
APPLICANT: Ruan, Xiaocan  
APPLICANT: Pereda-Lopez, Ana  
APPLICANT: Kakavas, Stephan J.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES  
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Rd.  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:

1 APPLICATION NUMBER: US/09/078,166  
2 FILING DATE: 16-MAY-1979  
3 CLASSIFICATION:  
4 PRIOR APPLICATION DATA:  
5 APPLICATION NUMBER:  
6 FILING DATE:  
7 ATTORNEY/AGENT INFORMATION:  
8 NAME: Dianne Casuto  
9 REGISTRATION NUMBER: P-40,943  
10 REFERENCE/DOCKET NUMBER: 4952.US.P2  
11 TELECOMMUNICATION INFORMATION:  
12 TELEPHONE: (847)-938-3137  
13 TELEFAX: (847)-938-2623  
14 TELEX:  
15 INFORMATION FOR SEQ ID NO: 32:  
16 SEQUENCE CHARACTERISTICS:  
17 LENGTH: 343 amino acids  
18 TYPE: amino acid  
19 STRANDEDNESS: single  
20 TOPOLOGY: linear  
21 MOLECULE TYPE: No. 6063561e  
22 US-09-078-166-32

Query Match 46.1%; Score 41; DB 3; Length 343;  
Best Local Similarity 46.7%; Pred. No. 41;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPLQVMEPQG 16  
1 1:11 1: 1:1  
DB 42 QLPRKLVLEPQG 56

RESULT 4  
US-08-997-467-32  
Sequence 32, Application US/08997467  
Patent No. 6200813  
GENERAL INFORMATION:  
APPLICANT: Katz, Leonard  
APPLICANT: Stassl, Diane L.  
APPLICANT: Summers Jr., Richard G.  
APPLICANT: Ruan, Xiaocan  
APPLICANT: Pereda-Lopez, Ana  
APPLICANT: Kakavas, Stephan J.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES  
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Rd.  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,467  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/858,003  
FILING DATE: 16-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne Casuto  
REGISTRATION NUMBER: P-40,943  
REFERENCE/DOCKET NUMBER: 4952.US.P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847)-938-3137  
TELEFAX: (847)-938-2623



	Query Match	Score	DB	Length
Db	Best Local Similarity	45.5%	40.5	369;
	Matches	9; Conservative	5; Mismatches	2; Indels
				3; Gaps
				1

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RESULT      9
US-09-121-321-16
: Sequence 16, Application US/09121321
: Patent No. 6090783
: GENERAL INFORMATION:
:   APPLICANT: Saiga, Akihiko
:   APPLICANT: Orita, Satoshi
:   APPLICANT: Igarashi, Hisanaga
:   APPLICANT: Okumura, Kouichi
:   APPLICANT: Sakaguchi, Gaku
: TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
:   TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: FISH & NEAVE
:   STREET: 1251 Avenue of the Americas
:   CITY: New York
:   STATE: New York
:   COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/121,321
:   FILING DATE:
:   CLASSIFICATION:
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US 08/933,803
:     FILING DATE: 19-SEP-1997
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Haley, James F.
:     REGISTRATION NUMBER: 27,794
:     REFERENCE/DOCKET NUMBER: SHGN-12C1P
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 212-596-9000
:     TELEFAX: 212-596-9090
:   INFORMATION FOR SEQ ID NO: 16:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 671 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:       MOLECULE TYPE: protein
: US-09-121-321-16

Query Match      44.9%: Score 40; DB 3; Length 671;
Best Local Similarity 57.1%; Pred. NO. 1.2e+02;
Matches      8; Conservative      1; Mismatches      5; Indels      0; Gaps      0;

QY      2 QTPQPLQVMEPQ 15
      1 111111:11
Db      415 QPQPQLQSPQPQ 428

RESULT      10
US-08-933-803A-16
: Sequence 16, Application US/08933803A
: Patent No. 6218522
: GENERAL INFORMATION:
:   APPLICANT: Saiga, Akihiko
:   APPLICANT: Orita, Satoshi

```

APPLICANT: Igarashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,803A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 671 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-933-803A-16

Query Match 44.9%; Score 40; DB 4; Length 671;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPPLQVMEPO 15  
DB 415 QPPQPOLQSQPOPO 428

RESULT 11  
US-08-858-207A-456  
Sequence 456, Application US/08858207A  
Patent No. 6348328  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Nicholas, Richard  
APPLICANT: Stodola, Robert  
TITLE OF INVENTION: No. 6348328e1 Compounds  
NUMBER OF SEQUENCES: 552  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A

FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmil, Edward R.  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 456:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6348328e  
US-08-858-207A-456

Query Match 43.3%; Score 38.5; DB 4; Length 179;  
Best Local Similarity 47.1%; Pred. No. 49;  
Matches 8; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 4 PPLQV--MMEPQD 17  
DB 88 PPLQVTSFGLPQD 104

RESULT 12  
US-09-297-937C-13  
Sequence 13, Application US/09297937C  
Patent No. 6337199  
GENERAL INFORMATION:  
APPLICANT: YUM, Do Young  
TITLE OF INVENTION: Membrane-Bound Glucanase Dehydrogenase, Gene Sequence  
TITLE OF INVENTION: Encoding the Same and Production of 2-Keto-D-Gluconate  
FILE REFERENCE: P66159USO  
CURRENT APPLICATION NUMBER: US/09/297,937C  
CURRENT FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: PCT/KR98/00296  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: KR 97-48802  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 1276  
TYPE: PRT  
ORGANISM: Erwinia cyrillipedi  
US-09-297-937C-13

Query Match 42.7%; Score 38; DB 4; Length 1276;  
Best Local Similarity 53.8%; Pred. No. 5.2e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPPPLQVME 13  
DB 826 LKNPGLVQAMMK 838

RESULT 13  
US-09-225-244-2  
Sequence 2, Application US/09225244  
Patent No. 6018038  
GENERAL INFORMATION:  
APPLICANT: Boung-Jun OH

```

; APPLICANT: Moon Kyung KO
; APPLICANT: Igor KOSTENYUK
; TITLE OF INVENTION: Incompatible Plant and Pathogen Interaction Related Gene
; FILE REFERENCE: 1942/35
; CURRENT APPLICATION NUMBER: US/09/225,244
; CURRENT FILING DATE: 1999-01-04
; EARLIER APPLICATION NUMBER: No. 6018038 Yet Assigned
; EARLIER FILING DATE: Concurrent Herewith
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Wordperfect 6.1 Windows
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Capsicum annuum
; us-09-225-244-2

Query Match      41.6%; Score 37; DB 3; Length 328;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 LGTPQPLQVMEPQG 16
      ::||| | | |
Db      27 VRKEPPLQANSDPNG 42

RESULT 14
US-09-417-242-2
; Sequence 2, Application US/09417242
; Patent No. 6252049
; GENERAL INFORMATION:
; APPLICANT: Bounng-Jun OH
; APPLICANT: Moon Kyung KO
; APPLICANT: Igor KOSTENYUK
; TITLE OF INVENTION: Incompatible Plant and Pathogen Interaction Related Gene
; FILE REFERENCE: 1942/35
; CURRENT APPLICATION NUMBER: US/09/417,242
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 09/225,244
; EARLIER FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Wordperfect 6.1 Windows
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Capsicum annuum
; US-09-417-242-2

Query Match      41.6%; Score 37; DB 4; Length 328;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 LGTPQPLQVMEPQG 16
      ::||| | | |
Db      27 VRKEPPLQANSDPNG 42

RESULT 15
US-08-194-468-2
; Sequence 2, Application US/08194468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montlun, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California

```

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; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-194-468-2

Query Match      41.0%; Score 36.5; DB 1; Length 2441;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

Qy      2 QTPQPLQ---VMEPQG 16
      ||||| | | | |
Db      1902 QTPQPAQPGSPVNMSPAG 1921

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Search completed: July 31, 2002, 15:23:44  
 Job time: 147 sec







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 31, 2002, 15:21:52 ; Search time 15.13 Seconds

(without alignments)  
107.966 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89

Sequence: 1 LGTPQPLQVMEPEQD 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	53.9	709	2	D86907
2	47.5	53.4	192	2	AP1753
3	46	51.7	639	2	S03268
4	46	51.7	693	2	B95032
5	46	51.7	693	2	B97903
6	44	49.4	134	2	S44430
7	44	49.4	134	2	S39046
8	44	49.4	137	2	I56498
9	44	49.4	671	2	C96534
10	43	48.3	134	2	AB0784
11	43	48.3	639	2	S13142
12	43	48.3	639	2	A60633
13	43	48.3	639	2	A56779
14	43	48.3	639	2	A56779
15	43	48.3	695	2	AE1406
16	43	48.3	699	2	AE1782
17	43	48.3	699	2	E97594
18	43	48.3	844	2	AC2816
19	43	48.3	844	2	AC2816
20	42	47.2	263	2	S74353
21	42	47.2	580	2	S13328
22	42	47.2	595	2	F85438
23	42	47.2	643	2	S55610
24	42	47.2	698	2	C82332
25	41	46.1	78	2	D91160
26	41	46.1	78	2	E65136
27	41	46.1	78	2	C86006
28	41	46.1	641	2	A24333
29	41	46.1	857	2	JN0800
					JC4169

30	41	46.1	1058	1	WMBE52	UL52 protein - hum
31	41	46.1	1653	2	B91052	hypothetical prote
32	41	46.1	1653	2	G65028	hypothetical prote
33	41	46.1	1653	2	F85896	hypothetical prote
34	40.5	45.5	549	2	S53427	protein-tyrosine-p
35	40.5	45.5	656	1	A55574	protein-tyrosine-p
36	40.5	45.5	656	1	JC4263	protein-tyrosine-p
37	40	44.9	237	2	G72676	hypothetical prote
38	40	44.9	259	2	T14439	hypothetical prote
39	40	44.9	282	2	T14440	hypothetical prote
40	40	44.9	284	2	T47277	lactoylgutathione
41	40	44.9	300	2	T21149	hypothetical prote
42	40	44.9	357	2	E96696	protein FIN21.10 l
43	40	44.9	357	2	T38405	hypothetical prote
44	40	44.9	380	2	H87344	esterase, probable
45	40	44.9	691	1	EFTWG	translation elonga

#### ALIGNMENTS

RESULT 1

D86907  
elongation factor G [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: D86907  
R:Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehr  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: D86907  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-709 <STO>  
A:Cross-References: GB:AE005176; PID:g12725331; PID:AAK06358.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: fusa  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homo

Query Match 53.9%; Score 48; DB 2; Length 709;  
Best Local Similarity 40.0%; Pred. No. 5.6;  
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGTPQPLQVMEPEQ 15  
DB 415 IEVPEVQLMVEPK 429

RESULT 2

AF1753  
ORF150 [bacteriophage bIL285] homolog Jln2571 [imported] - Listeria innocua (strain C1)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AF1753  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fshl,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluter, T.; Simoes, N.; Tilleret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AF1753  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <GLA>  
A:Cross-References: GB:AL592022; PID:CAAC97798.1; PID:g16415093; GSPDB:GN00178  
A:Experimental source: strain C1p11262  
C:Genetics:  
A:Gene: Jln2571

Query Match 53.4%; Score 47.5; DB 2; Length 192;  
Best Local Similarity 50.0%; Pred. No. 1.5;  
Matches 9; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

QY 3 TPQPL--LOYMPEQD 17  
DB 31 TPKPLPGVEISYEPQD 48

## RESULT 3

S03268  
tetraacycline resistance protein tetM - Ureaplasma urealyticum  
C/Species: Ureaplasma urealyticum  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 02-Feb-2001  
C/Accession: S03268  
R: Sanchez-Pescador, R.; Brown, J.T.; Roberts, M.; Urdea, M.S.  
Nucleic Acids Res. 16, 1216-1217, 1988  
A/Title: The nucleotide sequence of the tetraacycline resistance determinant tetM from U.  
A/Reference number: S03268; MUID:88144009  
A/Accession: S03268  
A/Molecule type: DNA  
A/Residues: 1-639 <SAN>  
A/Cross-references: GB:U08812; EMBL:X06901; NID:g475983; PIDN:AAA73978.1; PID:g475984  
C/Genetics:  
A/Gene: tetM  
A/Gene family: translation elongation factor G; translation elongation factor Tu homolog  
C/Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F/4131/Domain: translation elongation factor Tu homology <ETU>  
F/10-17/Region: nucleotide-binding motif A (P-loop)  
F/128-131/Region: GTP-binding NKXD motif  
F/220-222/Region: GTP-binding SAK/L motif  
F/16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #str

Query Match 51.7%; Score 46; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLQVMEP 14  
DB 339 IENHPILQIVPEP 352

## RESULT 4

B95032  
translation elongation factor G [imported] - Streptococcus pneumoniae (strain TIGR4)  
C/Species: Streptococcus pneumoniae  
C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C/Accession: B95032  
R: Mettlen, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A./Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.  
A/Reference number: A95000; MUID:11357209; PMID:11463916  
A/Accession: B95032  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-693 <NUR>  
A/Cross-references: GB:AE005672; PIDN:AAK74451.1; PID:g14971744; GSPDB:GN00164; TIGR:SP4  
A/Experimental source: strain TIGR4  
C/Genetics:  
A/Gene: SP0273  
C/Superfamily: translation elongation factor G; translation elongation factor Tu homolog

Query Match 51.7%; Score 46; DB 2; Length 693;  
Best Local Similarity 40.0%; Pred. No. 12;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQPLQVMEPQ 15  
DB 400 INVPEVYQLMEPK 414

## RESULT 5

B97903  
elongation factor G [imported] - Streptococcus pneumoniae (strain R6)  
C/Species: Streptococcus pneumoniae  
C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C/Accession: B97903  
R: Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; Dehoff, B.S.  
y, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.  
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A/Reference number: A97872; MUID:21429245; PMID:11544234  
A/Accession: B97903  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-693 <NUR>  
A/Cross-references: GB:AE007317; PIDN:AAK99054.1; PID:g15457799; GSPDB:GN00174  
C/Genetics:  
A/Gene: ftsA  
C/Superfamily: translation elongation factor G; translation elongation factor Tu homo

Query Match 51.7%; Score 46; DB 2; Length 693;  
Best Local Similarity 40.0%; Pred. No. 12;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQPLQVMEPQ 15  
DB 400 INVPEVYQLMEPK 414

## RESULT 6

S44430  
synuclein - human  
C/Species: Homo sapiens (man)  
C/Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 28-May-1999  
C/Accession: S44430  
R: Jakes, R.; Spillantini, M.G.; Goedert, M.  
FEBS Lett. 345, 27-32, 1994  
A/Title: Identification of two distinct synucleins from human brain.  
A/Reference number: S44430; MUID:94252398  
A/Accession: S44430  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-134 <JAK>  
A/Cross-references: GB:S69965; NID:g546911; PIDN:AAB30860.1; PID:g546912

Query Match 49.4%; Score 44; DB 2; Length 134;  
Best Local Similarity 46.2%; Pred. No. 4;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 QPLQVMEPEQD 17  
DB 105 EPLIEPLMEPEGE 117

## RESULT 7

S39046  
phosphonuroprotein 14 - bovine  
N/Alternate names: brain-specific protein, 14K  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 19-May-1994 #sequence\_revision 05-May-1995 #text\_change 05-May-1995  
C/Accession: S39046; MUID:238  
R: Nakajo, S.; Tsukada, K.; Ometa, K.; Nakamura, Y.; Nakaya, K.  
Eur. J. Biochem. 217, 1057-1063, 1993

A:Title: A new brain-specific 14-kDa protein is a phosphoprotein.. Its complete amino acid sequence is deduced from complementary DNA  
A:Reference number: S39046; MUID:94039126  
A:Accession: S39046  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-134 <NAK>  
R:Nakajo, S.; Tsunada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.  
Submitted to JPID, October 1993  
A:Description: A new brain-specific 14-kDa protein is a phosphoprotein: Its complete amino acid sequence is deduced from complementary DNA  
A:Reference number: JU0238  
A:Accession: JU0238  
A:Molecule type: protein  
A:Residues: 1-134 <NA2>  
I:Keywords: brain

Query Match	49.4%	Score 44	DB 2	Length 134
Best Local Similarity	46.2%	Pred. No. 4		
Matches	6	Conservative	6	Mismatches 1; Indels 0; Gaps 0;

```
QY      5 QPLQVMMERQGD 17
          :||: :|||:|:
Db     105 EPLIEPIMEPEGE 117
```

RESULT 8  
I56498  
phosphonuroprotein 14 - rat  
C:Species: Rattus sp. (rat)  
C:Date: 26-Jul-1996 #sequence.revision 26-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I56498  
R:ToBe, T.; Nakajo, S.; Tanaka, A.; Miotoya, A.; Omata, K.; Nakaya, K.; Tomita, M.; Nakam  
J. Neurochem. 59, 1624-1629, 1992  
A:Title: Cloning and characterization of the cDNA encoding a novel brain-specific 14-kDa  
A:Reference number: I56498; MUID:93019240  
A:Accession: I56498  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-137 <RMS>  
A:Cross-references: GB:DJ7764; NID:g409780; PIDN:BAA04610.1; PID:g459235

Query Match	49.4%	Score 44	DB 2	Length 137
Best Local Similarity	46.2%	Pred. No. 4.1		
Matches 6	Conservative 6	Mismatches 1	Indels 0	Gaps 0

```
QY      5 QPLLQVMEPQGD 17
          ::||::: |||::|:
Db     105 EPLIEPLMEPEGE 117
```

RESULT 9

C96534

probable Poly A Binding Protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

C:Accession: C96534

R:Theologios, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C96534

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-671 <STO>

A:Cross-references: GB:AE005173; NID:g10120431; PIDN:AAG13056.1; GSPDB:GN00141

C:Genetics:  
A:Gene: F14U22.3  
A:Map position: 1  
C:Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match	49.48;	Score 44;	DB 2;	Length 671;
Best Local Similarity	46.78;			
Matches	7;	Conservative	3;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
QY      2 QTPQPLLVMMEROG 16
          | | : : | | : |
Db      514 QQSPMMQQQMHPRG 528
```

RESULT 10  
AB0784  
conserved hypothetical protein STY2446 [imported] - *Salmonella enterica* subsp. *enterica*  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A:Note: This species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AB0784  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
S.; Moulé, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AB0784  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-134 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAPD02592.1; PID:g16503449; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2446

Query Match	48.3%	Score 43:	DB 2:	Length 134:
Best Local Similarity	61.5%	Pred, No.	5.9:	
Matches	8:	Conservative	1:	Mismatches 4:
				Indels 0:
				Gaps 0:

QY 2 QTPQLQVMEP 14  
| | | | | : |  
Db 63 QAPQLRQSM LSP 75

RESULT 11  
S13142  
tetracycline resistance protein tetM - Enterococcus faecalis transposon Tn916  
C:Species: Enterococcus faecalis  
C:Date: 13-Jan-1995 #sequence\_revision 10-Feb-1995 #text\_change 02-Feb-2001  
C:Accession: S13142  
R:Burdett, V.  
Nucleic Acids Res. 18, 6137, 1990  
A:Title: Nucleotide sequence of the tet(M) gene of Tn916.  
A:Reference number: S13142, MUID:91045089  
A:Accession: S13142  
A:Molecule type: DNA  
A:Residues: 1..639 <BGR>  
A:Cross-references: EMBL:X56353; NID:g47061; PIDN:CAA9796.1; PID:g47062  
R:Burdett, V.  
J. Biol. Chem. 266, 2872-2877, 1991  
A:Title: Purification and characterization of Tet(M), a protein that renders ribosome  
A:Reference number: A23749; MUID:91131580  
A:Contents: annotation; function; amino end of purified recombinant protein  
A:Note: protein purified after expression in E. coli shown to be ribosome-dependent G  
C:Genetics:  
A:Gene: tetM  
C:Superfamily: translation elongation factor G; translation elongation factor Tu hom  
C:Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-1loop  
F:4-131/Domain: translation elongation factor Tu homology <ETU>  
F:10-17/Region: nucleotide-binding motif A (P-1loop)

F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LQTPOLQVMEP 14  
Db 339 IENHPILQTTVEP 352

RESULT 12  
A60633  
tetacycline resistance protein - Staphylococcus aureus (strain MRSA101)  
C:Species: Staphylococcus aureus  
C>Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 02-Feb-2001  
C:Accession: A60633  
R:Nesin, M.; Svec, P.; Lupski, J.R.; Godson, G.N.; Kreiswirth, B.; Kornblum, J.; Projan, R.; Meslin, M.; Agents Chemother. 34, 2273-2276, 1990  
A:Title: Cloning and nucleotide sequence of a chromosomally encoded tetracycline resistance  
A:Reference number: A60633; MUID:91158314  
A:Accession: A60633  
A:Molecule type: DNA  
A:Residues: 1-639 <NES>  
A:Cross-references: GB:M21136; NID:q153114; PIDN:AAA26678.1; PID:q153115  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog  
C:Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F:4-131/Domain: translation elongation factor Tu homology <ETU>  
F:10-11/Region: nucleotide-binding motif A (P-loop)  
F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LQTPOLQVMEP 14  
Db 339 IENHPILQTTVEP 352

RESULT 13  
A56779  
tetacycline resistance protein TetM - Enterococcus faecalis transposon Tn916  
C:Species: Enterococcus faecalis  
C>Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 02-Feb-2001  
C:Accession: A56779  
R:Su, Y.A.; He, P.; Clewell, D.B.  
A:Antimicrob. Agents Chemother. 36, 769-778, 1992  
A:Title: Characterization of the tetM determinant of Tn916: evidence for regulation by  
A:Reference number: A56779; MUID:92368175  
A:Accession: A56779  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-639 <SU1>  
A:Cross-references: GB:M85225; NID:q148321; PIDN:AAA24784.1; PID:q148322  
C:Note: sequence extracted from NCBI backbone (NCBIN:111076, NCBIPI:111078)  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog  
C:Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F:4-131/Domain: translation elongation factor Tu homology <ETU>  
F:10-11/Region: nucleotide-binding motif A (P-loop)  
F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
OY 1 LQTPOLQVMEP 14  
Db 339 IENHPILQTTVEP 352

RESULT 14  
AE1406  
translation elongation factor G homolog fus [imported] - Listeria monocytogenes (stra  
C:Species: Listeria monocytogenes  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AE1406  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltounam, A.;  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1406  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-695 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAD00867.1; PID:q16412154; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: fus  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homo

Query Match 48.3% Score 43; DB 2; Length 695;  
Best Local Similarity 40.0%; Pred. No. 38;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQTPOLQVMEP 15  
Db 399 MEPEPVIOVAIEPK 413

RESULT 15  
AE1782  
translation elongation factor G homolog fus [imported] - Listeria innocua (strain C11  
C:Species: Listeria innocua  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AE1782  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltounam, A.;  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1782  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-695 <GLA>  
A:Cross-references: GB:M952022; PIDN:CAC98029.1; PID:q16415339; GSPDB:GN00178  
A:Experimental source: strain C11p11262  
C:Genetics:  
A:Gene: fus  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homo

Query Match 48.3% Score 43; DB 2; Length 695;  
Best Local Similarity 40.0%; Pred. No. 38;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQTPOLQVMEP 15  
Db 399 MEPEPVIOVAIEPK 413

Wed Jul 31 15:17:27 2002

us-09-641-802-2.rpr

Page 5

Search completed: July 31, 2002, 15:24:07  
Job time: 135 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 31, 2002, 15:23:47 ; Search time 10.34 Seconds  
(without alignments)  
63.659 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89

Sequence: 1 LQTPQLQLQVMMEPGD 17

Scoring table:

BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	53.9	691	1	ERG_STRPY
2	46	51.7	639	1	TETM_UREUR
3	44	47.2	134	1	SYUB_BOVIN
4	44	49.4	134	1	SYUB_HUMAN
5	44	49.4	137	1	SYUB_RAT
6	43	48.3	639	1	TETM_ENTFA
7	43	48.3	639	1	TETM_STRAU
8	43	48.3	639	1	TETM_STRAU
9	42	47.2	643	1	VP40_HSEVE
10	41	46.1	78	1	YHGG_ECOLI
11	41	46.1	544	1	TCPG_DROME
12	41	46.1	639	1	TETM_ENTFA
13	41	46.1	639	1	TETM_STRAU
14	41	46.1	641	1	TETM_LISMO
15	41	46.1	857	1	CAEP_THES7
16	41	46.1	857	1	CAEP_THES7
17	41	46.1	1058	1	UL52_HSV1
18	40	44.9	282	1	LGUL_BRAOL
19	40	44.9	357	1	YFQB_SCHPO
20	40	44.9	671	1	Z282_HUMAN
21	40	44.9	691	1	EFEG_SYNY3
22	40	44.9	691	1	EFEG_THETH
23	40	44.9	1161	1	POL_SFV1
24	39	43.8	249	1	GRPE_SYNY3
25	39	43.8	341	1	EFEG_STRRA
26	39	43.8	612	1	GAG_JSVRV
27	39	43.8	618	1	MTOL_HUMAN
28	39	43.8	639	1	TETM_NEIME
29	39	43.8	674	1	RNE_SYNY3
30	39	43.8	679	1	YKR8_YRST
31	39	43.8	708	1	EFGL_STRCO
32	39	43.8	758	1	PSAA_PEA
33	39	43.8	962	1	PTRA_ECOLI

34	39	43.8	1008	1	GALY_KLULA
35	39	43.8	1093	1	SM14_YEAST
36	39	43.8	1818	1	HMR2_MYCPN
37	39	43.8	2303	1	POLG_TWEVB
38	39	43.8	2303	1	POLG_TWEVB
39	39	43.8	2303	1	POLG_TWEVB
40	39	43.8	3344	1	POLG_PRSVH
41	38	42.7	167	1	YP74_MYCTU
42	38	42.7	691	1	EFEG_BACSU
43	38	42.7	694	1	EFEG_CHLMU
44	38	42.7	694	1	EFEG_CHLMU
45	38	42.7	697	1	EFEG_SPTPL
	38	42.7	699	1	EFEG_HAEIN

## ALIGNMENTS

RESULT 1  
ID ERG\_STRPY STANDARD; PRT; 691 AA.  
AC P82A77:  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Elongation factor G (EF-G).  
GN FUS OR SPY0273.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;  
RX MEDLINE-21192684; PubMed-11296296;  
RA Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
RN [2]  
RP PARTIAL SEQUENCE, AND MASS SPECTROMETRY.  
RC STRAIN-JRS4 / Serotype M6;  
RA Hogan D.A., Du P., Stevenson T.I., Whilton M., Kilby G.W., Rogers J.,  
RA VanBogelen R.A.;  
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
proteins.";  
RL Submitted (MAY-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION  
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE  
RIBOSOME (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-G/EF-2 SUBFAMILY.  
CC  
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the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AE006493; AKK3347.1; -.  
CC InterPro: IPR000640; EFG\_C.  
CC InterPro: IPR000795; GTP\_EFTU.  
CC InterPro: IPR004161; GTP\_EFTU\_D2.  
CC Pfam: PF006679; EFG\_C; 1.  
CC Pfam: PF00009; GTP\_EFTU; 1.  
CC Pfam: PF03144; GTP\_EFTU\_D2; 1.  
CC PRINTS: PR00315; ELONGATNCT.  
CC PROSITE: PS00301; EFATOR\_GTP; 1.  
CC Elongation factor; Protein biosynthesis; GTP-binding;

KW Complete proteome.  
 FT INT\_MET 0  
 FT NP\_BIND 16 23 GTP (BY SIMILARITY).  
 FT NP\_BIND 80 84 GTP (BY SIMILARITY).  
 FT NP\_BIND 134 137 GTP (BY SIMILARITY).  
 SQ SEQUENCE 691 AA; 76397 MW; D59B857ACDB40CD CAC64;

Query Match 53.9%; Score 48; DB 1; Length 691;  
 Best Local Similarity 40.0%; Pred. No. 1.9;  
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LOTPOPLQVMEPQ 15  
 Db 399 IEVPEVTLQVMEPK 413

RESULT 2  
 ID TERM\_UREUR STANDARD; PRT; 639 AA.  
 AC P09757;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tetracycline resistance protein tetM.  
 GN tetM.  
 OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=2130;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RA MEDLINE-8814409; PubMed-3344217;  
 RA Sanchez-Pescador R., Brown J.T., Roberts M., Urdea M.S.;  
 RT "The nucleotide sequence of the tetracycline resistance determinant  
 tetM from Ureaplasma urealyticum."  
 RL Nucleic Acids Res. 16:1216-1217(1988).  
 CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
 CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.  
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC TERM/ETO SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U08812; AAA73978.1; -;  
 DR PIR; S03268; S03268.  
 DR HSSP; P13551; IFNM.  
 DR InterPro: IPR000640; EFG\_C.  
 DR InterPro: IPR000795; GTP\_EFTU.  
 DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 DR Pfam; PF00679; EFG\_C; 1.  
 DR Pfam; PF00009; GTP\_EFTU; 1.  
 DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS; PR00315; ELONGATNCT.  
 DR PROSITE; PS00301; EFACOR\_GTP; 1.  
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.  
 FT NP\_BIND 10 17 GTP (BY SIMILARITY).  
 FT NP\_BIND 74 78 GTP (BY SIMILARITY).  
 FT NP\_BIND 128 131 GTP (BY SIMILARITY).  
 SQ SEQUENCE 639 AA; 72599 MW; A1497055BB182B3A CRC64;

Query Match 51.7%; Score 46; DB 1; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 3.8;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LOTPOPLQVMEP 14

Db 339 IENPPLQITVER 352

RESULT 3  
 ID SYUB\_BOVIN STANDARD; PRT; 134 AA.  
 AC P33567;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-synuclein (Phosphoneuroprotein 14) (PMP 14) (14 kDa brain-  
 DE specific protein).  
 GN SNCA.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE-94039126; PubMed-823629;  
 RA Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;  
 RT "A new brain-specific 14-kDa protein is a phosphoprotein. Its  
 RT complete amino acid sequence and evidence for phosphorylation."  
 RL Eur. J. Biochem. 217:1057-1063(1993).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE-91038084; PubMed-2230807;  
 RA Nakajo S., Omata K., Aichi T., Shibayama T., Okahashi I., Ochiai H.,  
 RA Nakai Y., Nakaya K., Nakamura Y.;  
 RT "Purification and characterization of a novel brain-specific 14-kDa  
 RT protein."  
 RL J. Neurochem. 55:2031-2038(1990).  
 CC -1- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY PRESENT IN SYNAPSES AROUND  
 CC NEURONS BUT NOT IN GLIAL CELLS.  
 CC -1- PTM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR  
 CC KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2  
 CC AND CAM-KINASE II (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.  
 CC -----  
 DR PIR; A60218; A60218.  
 DR PIR; J00238; J00238.  
 DR PIR; S39046; S39046.  
 DR InterPro: IPR001058; Synuclein.  
 DR Pfam; PF01387; Synuclein; 1.  
 DR PRODOM; PD010631; Synuclein.  
 KW Phosphorylation; Repeat.  
 FT DOMAIN 20 67  
 FT REPEAT 20 30  
 FT REPEAT 31 41  
 FT REPEAT 42 56  
 FT REPEAT 57 67  
 FT MOD\_RRS 118 118  
 SQ SEQUENCE 134 AA; 14277 MW; 484FA01A01979966 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 134;  
 Best Local Similarity 46.2%; Pred. No. 1.5;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 5 QPLIQVMEPQGD 17  
 Db 105 EPLIEPLMEPEGE 117

RESULT 4



SYUB\_HUMAN  
ID SYUB\_HUMAN STANDARD: PRT; 134 AA.  
AC 016143;  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 16-OCT-2001 (rel. 40, Last annotation update)  
DE Beta-synuclein.  
GN SMCB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94252398; PubMed=8194594;  
RA Jakes R., Spillantini M.G., Goedert M.;  
RT "Identification of two distinct synucleins from human brain.";  
RL FEBS Lett. 345:27-32(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99026142; PubMed=9806846;  
RA Lavedan C., Leroy E., Torres R., Dehejia A., Dutra A., Buchholtz S.,  
RA Nussbaum R.L., Polymeropoulos M.H.;  
RT "Genomic organization and expression of the human beta-synuclein gene  
(SNCA).";  
RL Genomics 54:173-175(1998).  
RN [3]  
RP PHOSPHORYLATION.  
RX MEDLINE=20409007; PubMed=10852916;  
RA Pronin A.N., Morris A.J., Surguchov A., Benovic J.L.;  
RT "Synucleins are a novel class of substrates for G protein-coupled  
receptor kinases.";  
RL J. Biol. Chem. 275:26515-26522(2000).  
CC -1- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN; CONCENTRATED  
CC IN PRESYNAPTIC NERVE TERMINALS.  
CC -1- PTM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR  
CC KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2  
CC AND CAM-KINASE II.  
CC -1- DISEASE: BRAIN IRON ACCUMULATION TYPE 1 (NBIA1), ALSO CALLED  
CC HALLERVOEDEN-SPATZ SYNDROME), A RARE NEUROAXONAL DYSTROPHY, IS  
CC HISTOLOGICALLY CHARACTERIZED BY AXONAL SPHEROIDS, IRON DEPOSITION,  
CC LEWY BODY (LB)-LIKE INTRANEURONAL INCLUSIONS, GLIAL INCLUSIONS AND  
CC NEUROFIBRILLARY TANGLES. SMCB IS FOUND IN SPHEROIDS BUT NOT IN  
CC INCLUSIONS.  
CC -1- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.  
CC -----  
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CC -----  
CC EMBL: S69965; AAC30860.1;  
CC EMBL: AF053136; AAC80286.1;  
CC EMBL: AF053134; AAC80286.1; JOINED.  
CC EMBL: AF053135; AAC80286.1; JOINED.  
CC MIM: 602569;  
CC DR InterPro: IPR001058; Synuclein.  
CC DR Pfam: PF01387; Synuclein.1.  
CC DR PRINTS: PRO1211; SYNUCLEIN.  
CC DR ProDom: PD010631; Synuclein.1.  
CC DR Phosphorylation: Repeat.  
CC KW DOMAIN 20 67  
CC FT 4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-  
CC [EQ]-[GQ]-V-X(4).  
CC FT REPEAT 20 30 1.  
CC FT REPEAT 31 41 2.  
CC FT REPEAT 42 56 3 (APPROXIMATE).  
CC FT REPEAT 57 67 4.

FT MOD\_RES 118 118 PHOSPHORYLATION (BY CK2, GKR2 AND GKR5).  
SQ SEQUENCE 134 AA; 14288 MW; 5BCA9FCA615AC4EF CRC64;  
Query Match 49.4%; Score 44; DB 1; Length 134;  
Best Local Similarity 46.2%; Pred. No. 1.5;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 5 OPILOVMEPOGD 17  
Db 105 EPLIPLMEPEGE 117  
RESULT 5  
SYUB\_RAT  
ID SYUB\_RAT STANDARD: PRT; 137 AA.  
AC 063754;  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 16-OCT-2001 (rel. 40, Last annotation update)  
DE Beta-synuclein (phosphonucleoprotein 14) (PMP 14).  
GN SMCB.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93019240; PubMed=1402909;  
RA Toke T., Nakajo S., Tanaka A., Mitoa A., Omata K., Nakaya K.,  
RA Tomita M., Nakamura Y.;  
RT "Cloning and characterization of the cDNA encoding a novel brain-  
specific 14-kDa protein.";  
RL J. Neurochem. 59:1624-1629(1992).  
RN [2]  
RP PHOSPHORYLATION BY CAM-KINASE II.  
RX MEDLINE=94039126; PubMed=8223629;  
RA Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;  
RT "A new brain-specific 14-kDa protein is a phosphoprotein. Its complete  
RT amino acid sequence and evidence for phosphorylation.";  
RL Eur. J. Biochem. 217:1057-1063(1993).  
CC -1- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.  
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN BRAIN.  
CC -1- PTM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR  
CC KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2  
CC AND CAM-KINASE II.  
CC -1- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.  
CC -----  
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CC -----  
CC EMBL: D17764; BAA04610.1;  
CC DR InterPro: IPR001058; Synuclein.  
CC DR Pfam: PF01387; Synuclein.1.  
CC DR PRINTS: PRO1211; SYNUCLEIN.  
CC DR ProDom: PD010631; Synuclein.1.  
CC DR Phosphorylation: Repeat.  
CC KW DOMAIN 20 67  
CC FT 4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-  
CC [EQ]-[GQ]-V-X(4).  
CC FT REPEAT 20 30 1.  
CC FT REPEAT 31 41 2.  
CC FT REPEAT 42 56 3 (APPROXIMATE).  
CC FT REPEAT 57 67 4.  
CC FT MOD\_RES 118 118 PHOSPHORYLATION (BY CK2, GKR2 AND GKR5)  
CC (BY SIMILARITY).  
SQ SEQUENCE 137 AA; 14504 MW; 678C6CB84FA01A03 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 137;  
 Best Local Similarity 46.2%; Pred. No. 1.5;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 QPLQVMEPEOGD 17

DB 105 EPLIEPLMEPEGE 117

RESULT 6

TEP9\_ENTFA

ID TEP9\_ENTFA

AC P21598;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tetracycline resistance protein tetM from transposon Tn916

GN (tetM(916)).

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;

OC Enterococcus.

OX NCBI\_TaxID=1351;

RN NCBI\_TaxID=1351;

RP [1]

SEQUENCE FROM N.A.

RC TRANSPOSON-Tn916;

RX MEDLINE=91045089; PubMed=2172929;

RA Burdett V.;

RT "Nucleotide sequence of the tet(M) gene of Tn916."

RL Nucleic Acids Res. 18:6137-6137(1990).

CC - FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN

CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.

CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

CC TETM/TETO SUBFAMILY.

CC -----

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CC -----

CC DR EMBL; X56353; CAA39796.1; -

DR PIR; S13142; S13142.

DR HSSP; P13551; IFNM.

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam; PF00679; EFG\_C; 1.

DR Pfam; PF00009; GTP\_EFTU; 1.

DR Pfam; PF03144; GTP\_EFTU\_D2; 1.

DR PRINTS; PR00315; ELONGATNFC.

DR PROSITE; PS00301; EFACOR\_GTP; 1.

KW Protein biosynthesis; Antibiotic resistance; GTP-binding;

KW Transposable element.

FT NP\_BIND 10 17 GTP (BY SIMILARITY).

FT NP\_BIND 74 78 GTP (BY SIMILARITY).

FT NP\_BIND 128 131 GTP (BY SIMILARITY).

SEQUENCE 639 AA; 72464 MW; B2315A37B53B18FB CRC64;

QY 1 LQTPQPLQVMEPE 14

DB 339 IENHPPLQVTEP 352

RESULT 7

Query Match 48.3%; Score 43; DB 1; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

TETM\_STAUI STANDARD; PRT; 639 AA.

ID TETM\_STAUI

AC O53770;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Tetracycline resistance protein tetM (tetM(M)).

GN TETM OR TETM(M).

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Staphylococcus.

OX NCBI\_TaxID=1280;

RN NCBI\_TaxID=1280;

RP [1]

SEQUENCE FROM N.A.

RX MEDLINE=91158314; PubMed=2073121;

RA Nesin M., Svec P., Lupski J.R., Godson G.N., Kreiswirth B.,

Projan S.J.;

RT "Cloning and nucleotide sequence of a chromosomally encoded

tetracycline resistance determinant, tet(M), from a pathogenic,

methicillin-resistant strain of Staphylococcus aureus."

RL Antimicrob. Agents Chemother. 34:2273-2276(1990).

CC - FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN

CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.

CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

CC TETM/TETO SUBFAMILY.

CC -----

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CC -----

CC DR EMBL; M21136; AAA26678.1; -

DR HSSP; P13551; IFNM.

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam; PF00679; EFG\_C; 1.

DR Pfam; PF00009; GTP\_EFTU; 1.

DR Pfam; PF03144; GTP\_EFTU\_D2; 1.

DR PRINTS; PR00315; ELONGATNFC.

DR PROSITE; PS00301; EFACOR\_GTP; 1.

KW Protein biosynthesis; Antibiotic resistance; GTP-binding.

KW NP\_BIND 10 17 GTP (BY SIMILARITY).

FT NP\_BIND 74 78 GTP (BY SIMILARITY).

FT NP\_BIND 128 131 GTP (BY SIMILARITY).

SEQUENCE 639 AA; 72639 MW; 66470062A673BE1F CRC64;

QY 1 LQTPQPLQVMEPE 14

DB 339 IENHPPLQVTEP 352

RESULT 8

EFG\_AGRU

ID EFG\_AGRU

AC P70782;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Elongation factor G (EF-G).

GN FUSA.

OS Agrobacterium tumefaciens.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI\_TaxID=358;

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RN [1]
SEQUENCE FROM N.A.
RX MEDLINE-97047977; PubMed-8892818;
RA Syvonen A., Amiri H., Jamel A., Andersson S.G.E., Kurland C.G.;
RT "A chimeric disposition of the elongation factor genes in Rickettsia
  prowazekii."
RL J. Bacteriol. 178:6192-6199(1996).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
  OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
  RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
DR EMBL: X99673; CA67990.1; -.
DR HSSP: P13551; IFNM.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C.1.
DR Pfam: PF00009; GTP_EFTU.1.
DR Pfam: PF03144; GTP_EFTU_D2.1.
DR PROSITE: PS00301; EFACITOR_GTP.1.
KM Elongation factor; Protein biosynthesis; GTP-binding.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 86 90 GTP (BY SIMILARITY).
FT NP_BIND 140 143 GTP (BY SIMILARITY).
SQ SEQUENCE 699 AA; 78044 MW; E72A1081DEC28E2B CRC64;

Query Match 48.3%; Score 43; DB 1; Length 699;
Best Local Similarity 36.8%; Pred. No. 13;
Matches 7; Conservative 8; Mismatches 2; Indels 2; Gaps 1;

OY 1 LQTPQLQVMMEP--QGD 17
DB 406 MEPEVIOIAIEPKTKGD 424

RESULT 9
VP40_HSV2 STANDARD; PRT; 643 AA.
AC P52369;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Capsid protein P40 [Contains: Assemblin (Protease) (EC 3.4.21.97);
  DE Capsid assembly protein].
GN 17
OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OC NCBI_TaxID=82831;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95302501; PubMed-7783207;
RA Telford E.A., Watson M.S., Alid H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2."
RL J. Mol. Biol. 249:520-528(1995).
CC -1- FUNCTION: THE CAPSID ASSEMBLY PROTEIN IS COMPONENT OF THE CAPSID
  CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA.
CC -1- FUNCTION: ASSEMBLIN IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE
  ITSELF AND THE CAPSID ASSEMBLY PROTEIN AT THE C-TERMINUS.
CC -1- CATALYTIC ACTIVITY: PREFERENTIALLY CLEAVES AT ALA-I-SER OR ALA-I-
  ALA.

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CC -1- CATALYTIC ACTIVITY: CLEAVES -ALA + SER- AND -ALA + ALA- BONDS IN
  THE SCAFFOLD PROTEIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21 (SERINE PROTEASE).
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
CC -----
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CC -----
DR EMBL: U20824; AAC13804.1; -.
DR HSSP: P16753; ICMV.
DR MEROPS: S21.001; -.
DR InterPro: IPR001847; Assemblin.
DR Pfam: PF00716; Peptidase_S21.1.
KM Coat protein; Hydrolyase; Serine protease.
FT CHAIN 1 269 ASSEMBLIN (PROTEASE).
FT CHAIN 270 643 CAPSID ASSEMBLY PROTEIN.
FT SITE 269 270 CLEAVAGE (BY THE PROTEASE) (PROBABLE).
FT ACT_SITE 82 82 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 643 AA; 68394 MW; 1108A7A40E9FCA38 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 643;
Best Local Similarity 57.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 QTPQLQVMMEPQ 15
DB 486 QEPQLPQPQLPQ 499

RESULT 10
YHGG_ECOLI STANDARD; PRT; 78 AA.
AC P46845;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yhgg.
DE YHGG OR B3410 OR Z4765 OR EC54252.
GN YHGG
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
  RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
  RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
  RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
  RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
  RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
  RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
  RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).

```

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-0157:H7 / RIMD 0509952;  
 RX MEDLINE-21156231; PubMed-11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K.,  
 Han C.-G., Ohtsubo H., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 Kohata S., Shiba T., Hattori M., Shinagawa H.;  
 RT Complete genome sequence of enterohemorrhagic *Escherichia coli*  
 O157:H7 and genomic comparison with a laboratory strain K-12.\*;  
 RL DNA Res. 8:11-22(2001).  
 CC -----  
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 CC -----  
 CC EMBL: U18997; AAA58208.1; -;  
 DR EMBL: AE000416; AAC76435.1; -;  
 DR EMBL: AE005563; AAG58511.1; -;  
 DR EMBL: AP002565; BAB37675.1; -;  
 DR EcoGene: EC12933; yhgC.  
 KW Hypothetical protein, Complete proteome.  
 SQ SEQUENCE 78 AA; 8660 MW; 8897bDE22CA9024B CRC64;

Query Match 46.1%; Score 41; DB 1; Length 78;  
 Best Local Similarity 46.2%; Pred. No. 2.6;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGTPOPLQVME 13  
 Db 26 LMTPOPMINMLQ 38

RESULT 11  
 TPCG\_DROME STANDARD; PRT; 544 AA.  
 AC P48605; O9VER9;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma).  
 GN CCT-GAMMA OR CCT-3 OR CCG OR CG8977.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Phryganea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON-S.  
 RA Martin C.H., Mayeda C.A., Davis C.A., Eriasson C.L., Kafets J.D.,  
 Mathog D.R., Celinker S.E., Lewis E.B., Palazzolo M.J.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96257223; PubMed-8666276;  
 RA Walkley N.A., Malik A.N.;  
 RT "Drosophila melanogaster P1 genomic clone DS05563 contains the  
 RL chaparonein-encoding gene Ccpg.";  
 RL Gene 171:221-223(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abail J.F., Abdyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnetl A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleab J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs X.H., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON  
 CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF  
 CC ACTIN AND TUBULIN.  
 CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT  
 CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.

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 CC -----  
 CC EMBL: U31961; AAA84416.1; -;  
 DR EMBL: X95602; CAA64860.1; -;  
 DR EMBL: AE003714; AAF55350.1; -;  
 DR HSSP: P48424; 1A6D.  
 DR FlyBase: FBgn0015019; CCT-gamma.  
 DR InterPro: IPR002423; TCP1\_cpnb60.  
 DR InterPro: IPR002194; TCP\_1.  
 DR Pfam: PF00118; cpnb60\_TCP1\_1.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00750; TCP1\_1; 1.  
 DR PROSITE: PS00751; TCP1\_2; 1.  
 DR PROSITE: PS00995; TCP1\_3; 1.  
 KW Chaperone; ATP-binding; Multigene family.  
 FT CONFLICT 12 12 S -> SD (IN REF. 2).  
 FT CONFLICT 35 47 MISSING (IN REF. 1).  
 SQ SEQUENCE 544 AA; 59394 MW; DD5E635809B322C2 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 544;  
 Best Local Similarity 46.2%; Pred. No. 22;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 44 POA.MKLM.DPMG 56

RESULT 12  
TETS\_ENTFA STANDARD: PRT: 639 AA.

DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tetracycline resistance protein tetM from transposon Tn1545  
(TetM(1545)).  
GN TETM OR TET(M).

OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
OC Enterococcus.

OX NCBI\_TaxId=1351;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-BM4127; TRANSPOSON-Tn1545;  
RX MEDLINE=87016342; PubMed=3020504;

RA Martin P., Trieu-Cuot P., Courvalin P.;  
RT "Nucleotide sequence of the tetM tetracycline resistance determinant  
of the streptococcal conjugative shuttle transposon Tn1545.";

RL Nucleic Acids Res. 14:7047-7058(1986).

CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.

CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC TETM/TETO SUBFAMILY.

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DR EMBL: X04388; CAA2977.1; -  
DR PIR: A24333; A24333.

DR HSSP: P1351; 1FNM.

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam: PF00679; EFG\_C.1.

DR Pfam: PF00009; GTP\_EFTU.1.

DR Pfam: PF03144; GTP\_EFTU\_D2.1.

DR PRINTS: PR00315; ELONGATNFCF.

DR PROSITE: PS00301; EFACOR\_GTP.1.

KW Protein biosynthesis; Antibiotic resistance; GTP-binding;  
KW Transposable element.

KM Transposable element.

FT NP\_BIND 10 17 GTP (BY SIMILARITY).

FT NP\_BIND 74 78 GTP (BY SIMILARITY).

FT NP\_BIND 128 131 GTP (BY SIMILARITY).

SO SEQUENCE 639 AA; 72657 MW; 2F7A3CD0588253CE CRC64;

Query Match 46.1%; Score 41; DB 1; Length 639;  
Best Local Similarity 50.0%; Pred. No. 26;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LOTPOPLQVMMEP 14  
DB 339 IENPLPLQTVVEP 352

RESULT 13  
TETM\_STRPN STANDARD: PRT: 639 AA.  
AC 054807;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Tetracycline resistance protein tetM from transposon Tn5251 (Tet(M)).  
GN TETM(5251).

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OC Streptococcus.

OX NCBI\_TaxId=1313;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-DP 1322;

RX MEDLINE=96162866; PubMed=8595862;

RA Provvedi R., Manganello R., Pozzi G.;

RT "Characterization of conjugative transposon Tn5251 of Streptococcus  
pneumoniae.";

CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.

CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC TETM/TETO SUBFAMILY.

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DR EMBL: X90939; CAA62436.1; -  
DR HSSP: P1351; 1FNM.

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam: PF00679; EFG\_C.1.

DR Pfam: PF00009; GTP\_EFTU.1.

DR Pfam: PF03144; GTP\_EFTU\_D2.1.

DR PRINTS: PR00315; ELONGATNFCF.

DR PROSITE: PS00301; EFACOR\_GTP.1.

KW Protein biosynthesis; Antibiotic resistance; GTP-binding;  
KW Transposable element.

FT NP\_BIND 10 17 GTP (BY SIMILARITY).

FT NP\_BIND 74 78 GTP (BY SIMILARITY).

FT NP\_BIND 128 131 GTP (BY SIMILARITY).

SO SEQUENCE 639 AA; 72556 MW; F18131E08881F3C0 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 639;  
Best Local Similarity 50.0%; Pred. No. 26;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LOTPOPLQVMMEP 14  
DB 339 IENPLPLQTVVEP 352

RESULT 14  
TETS\_LISMO STANDARD: PRT: 641 AA.  
AC 048791;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Tetracycline resistance protein tets (Tet(S)).  
GN TETS OR TET(S).

OS Listeria monocytogenes.  
OG Plasmid pIB811.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.

OX NCBI\_TaxId=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BM4210;  
RX MEDLINE=93380670; PubMed=8370538;











Db 415 IEVPEVITQLVMEPK 429

RESULT 2

0928G4 PRELIMINARY; PRT; 192 AA.

AC 0928G4; (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE LIN2571. PROTEIN.

GN LIN2571.

OS *Listeria innocua*.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Listeria.

OX NCBI\_TaxID=1642;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CLIP 11262 / SEROVAR 6A;

RX PubMed-11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Cherouani F., Couve E., de Darvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurge O.,

RA Ertian K.-D., Esht H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Kreft J., Kunst F., Kurapkt G.,

RA Madueno E., Malouin A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordstedt G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,

RA Rammel B., Rose M., Schluter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Weiland J., Cozzari F.,

RT "Comparative genomics of *Listeria* species."

RL Science 294:849-852(2001).

DR EMBL: AL596172; CAC97798.1;

DR Listlist: LIN02571;

KW Complete proteome.

SO SEQUENCE 192 AA; 20841 MW; BEBA4BD3261DDA74 CRC64;

Query Match 53.4%; Score 47.5; DB 16; Length 192;

Best Local Similarity 50.0%; Pred. No. 3.5;

Matches 9; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

OY 3 TPQPL---LOYMEPEQD 17

Db 31 TPKPLPGVEISVPEQD 48

RESULT 3

097503 PRELIMINARY; PRT; 693 AA.

AC 097503; (TREMBlrel. 18, Created)

DT 01-DEC-2001 (TREMBlrel. 18, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE TRANSLATION ELONGATION FACTOR G.

GN SP0273.

OS *Streptococcus pneumoniae*.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TIGR4;

RC MEDLINE-21357209; PubMed-11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,

RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Raddue D.,

RA Holtzapfe E., Khouri H., Wolf A.M., Uitterback T.R., Hansen C.L.,

RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickenson T., Hickey E.K.,

RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

RT "Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*."

RL Science 293:498-506(2001).

DR EMBL: AE007340; AKK74451.1;

DR TIGR: SP0273;

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam: PF00679; EFG\_C.1.

DR Pfam: PF00009; GTP\_EFTU.1.

DR Pfam: PF03144; GTP\_EFTU\_D2.1.

DR PRINTS: PR00315; ELONGACTNCT.

DR PROSITE: PS00301; EFCTOR\_GTP.1.

KW Elongation factor; Complete proteome.

SO SEQUENCE 693 AA; 76831 MW; 73187D0287AC6193 CRC64;

Query Match 51.7%; Score 46; DB 16; Length 693;

Best Local Similarity 40.0%; Pred. No. 23;

Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQTPPLQVMEPEQ 15

Db 400 INVEPEVITQLVMEPK 414

RESULT 4

035745 PRELIMINARY; PRT; 667 AA.

AC 035745; (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE ZINC FINGER PROTEIN REGULATOR OF APOPTOSIS AND CELL CYCLE ARREST.

GN ZAC1.

OS *Mus musculus* (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-PITUITARY GLAND;

RC MEDLINE-97327559; PubMed-9184226;

RA Spengler D., Villalba M., Hoffmann A., Pantalon C., Housami S.,

RA Bockaert J., Journot L.,

RT "Regulation of apoptosis and cell cycle arrest by Zac1, a novel zinc finger protein expressed in the pituitary gland and the brain."

RL EMBO J. 16:2814-2825(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-PITUITARY GLAND;

RA Spengler D., Villalba M., Hoffmann A., Pantalon C., Housami S.,

RA Bockaert J., Journot L.,

CC Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL: X95503; CAA64757.1;

DR EMBL: X95504; CAA64758.1;

DR MGD: MGI:1100874; Zac1.

DR InterPro: IPR000822; ZnF-C2H2.

DR Pfam: PF00096; ZnF-C2H2.7.

DR PRINTS: PR00048; ZNCFINGER.

DR SMART: SM00355; ZnF\_C2H2.7.

DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 7.

DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.

KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.

SO SEQUENCE 667 AA; 75258 MW; 392F0AC979C8C10F CRC64;

Query Match 50.6%; Score 45; DB 11; Length 667;

Best Local Similarity 60.0%; Pred. No. 32;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LQTPPLQVMEPEQ 15

Db 543 LPVQPLPQPOMOPO 557

## RESULT 5

09EPT3 PRELIMINARY; PRT; 675 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE LOST ON TRANSFORMATION PROTEIN 1.  
 GN ZAC1 OR LOT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH-SWISS;  
 RX MEDLINE=20065118; PubMed=10597250;  
 RA Abdollahi A., Bao R., Hamilton T.C.;  
 RT "LOT1 is a growth suppressor gene down-regulated by the epidermal  
 growth factor receptor ligands and encodes a nuclear zinc-finger  
 protein.";  
 RT Oncogene 18:6477-6487(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH-SWISS;  
 RA Abdollahi A., Hamilton T.C.;  
 RT "Identification of a splice variant of mouse Lot1 gene.";  
 RT Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF324471; ANG48331.1;  
 DR MGD: MGI:1100874; Zacl.  
 DR InterPro: IPR000822; Znf-C2H2.  
 DR Pfam: PF00096; Zf-C2H2; 7.  
 DR SMART: SM00355; Znf\_C2H2; 7.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.  
 DR DNA-binding; Metal-binding; Zinc-finger.  
 KW SEQUENCE 675 AA; 76109 MW; 0F467D165CA5B097 CRC64;

## Query Match

Best local Similarity 50.6%; Score 45; DB 11; Length 675;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LQTPQPLQVMEPO 15

Db 540 LPVQPLPQPOMOPO 554

## RESULT 6

09JLQ4 PRELIMINARY; PRT; 704 AA.

DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ZINC FINGER PROTEIN ZAC1.  
 GN ZAC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20136063; PubMed=10669760;  
 RA Huang S.-M., Stallcup M.R.;  
 RT "Mouse Zacl, a Transcriptional Coactivator and Repressor for Nuclear  
 Receptors.";  
 RT Mol. Cell. Biol. 20:1855-1867(2000).  
 DR EMBL: AF147785; AAF34245.1; -

DR MGD: MGI:1100874; Zacl.  
 DR InterPro: IPR000822; Znf-C2H2.  
 DR Pfam: PF00096; Zf-C2H2; 7.  
 DR SMART: SM00355; Znf\_C2H2; 7.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.  
 DR DNA-binding; Metal-binding; Zinc-finger.  
 KW SEQUENCE 704 AA; 79214 MW; 3AF88262D504FA80 CRC64;

OY 1 LQTPQPLQVMEPO 15

Db 543 LPVQPLPQPOMOPO 557

Query Match 50.6%; Score 45; DB 11; Length 704;  
 Best local Similarity 60.0%; Pred. No. 34;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

## RESULT 7

091Z23 PRELIMINARY; PRT; 133 AA.

DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE BETA-SYNOCLEIN.  
 GN SNCB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21367613; PubMed=11474193;  
 RA Sopher B.L., Koszidin K.L., McClain M.E., Myrick S.B., Martinez R.A.,  
 RA Smith A.C., La Spada A.R.;  
 RT "Genomic organization, chromosome location, and expression analysis of  
 mouse beta-synuclein, a candidate for involvement in  
 neurodegeneration.";  
 RL Cytogenet. Cell Genet. 93:117-123(2001).  
 DR EMBL: AF348164; AAK83238.1;  
 DR EMBL: AF348162; AAK83238.1; JOINED.  
 DR EMBL: AF348163; AAK83238.1; JOINED.  
 KW SEQUENCE 133 AA; 14052 MW; 8274D8A6A0D8E4D5 CRC64;

## Query Match

Best local Similarity 49.4%; Score 44; DB 11; Length 133;

Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 5 QPLQVMEPOGD 17

Db 104 EPLIEPLMEPEGE 116

## RESULT 8

090538 PRELIMINARY; PRT; 182 AA.

DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE MERZOITTE SURFACE PROTEIN 1 (FRAGMENT).  
 GN MSP-1.  
 OS Plasmodium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RPV97-73;  
 RA Kim S.H., Kwon S.I.;  
 RT "Analysis of the Plasmodium vivax merozoite surface protein 1 gene

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RT sequence from resurgent Korean isolates."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-KPV97-73;
RA Lee K.N., Song K.J., Song J.W., Lim C.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098282; AAF25530.1; -
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19514 MW; 2BB8A7A12D4471C5 CRC64;

Query Match 49.4%; Score 44; DB 5; Length 182;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMEPQD 17
Db 56 QQPQSQVVPAPAGD 71

RESULT 9
OQ9N959 PRELIMINARY; PRT; 227 AA.
AC OQ9N959;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POSSIBLE HYPOTHETICAL 14.6 KDA PROTEIN.
GN CHRL.04.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_Taxid=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRE0927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL559782; CAB95318.1; -
SQ SEQUENCE 227 AA; 26099 MW; AAF344E1959DD1E3 CRC64;

Query Match 49.4%; Score 44; DB 5; Length 227;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMEPQ 15
Db 48 QIPQSVLOVLOEPR 61

RESULT 10
OQ9FA2 PRELIMINARY; PRT; 671 AA.
AC OQ9FA2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE POLY-A BINDING PROTEIN.
GN F14J22.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremetskaya I., Kim C., Lenz C., Li J., Liu S.,

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RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaya V.S.,
RA Walker M., Yu G., Ecker J., Theologos A., Davis R.W.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologos A., Davis R.W.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011807; AAG13056.1; -
DR EMBL; AF370517; AAK43894.1; -
DR HSSP; P11940; ICVJ.
DR InterPro: IPR002343; Hud_Sxl_RNA.
DR InterPro: IPR002004; PABP.
DR InterPro: IPR005054; RRM.
DR InterPro: IPR003954; RRM.1.
DR Pfam; PF00658; PABP. 1.
DR PRINTS; PR00961; HUDSLRNA.
DR SMART; SM00360; RRM; 4.
DR SMART; SM00361; RRM_1; 4.
DR PROSITE; PS50102; RRM; 4.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 671 AA; 72779 MW; 49712E533BD4E55 CRC64;

Query Match 49.4%; Score 44; DB 10; Length 671;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMEPQ 16
Db 514 QQPSPMMQOQMHPRG 528

RESULT 11
OQ9S4T6 PRELIMINARY; PRT; 252 AA.
AC OQ9S4T6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TETRACYCLINE RESISTANCE PROTEIN (FRAGMENT).
GN TETM.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRNG 400;
RA Ferreira E., Louro D., Gomes J.P., Catry M.A., Vaz Pato M.V.;
RL Surveillance of tetracycline-resistant gonococci in Lisbon. Isolation
of a TRNG strain with tetracycline MIC=2 mg/L."
DR EMBL; AF116348; AAD48368.1; -
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
KM Cyclin; GTP-binding. 1
FT NON_TER 1
FT NON_TER 252
SQ SEQUENCE 252 AA; 29007 MW; 25B846A2F2BDC067 CRC64;

Query Match 48.3%; Score 43; DB 2; Length 252;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 LQTPOLQVMMMP 14  
 DB 234 IENPHPLQTVTEP 247

RESULT 12

094103 PRELIMINARY; PRT; 472 AA.  
 AC 094103:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 GN POLYADENYLATED MRNA-BINDING PROTEIN 2 (FRAGMENT).  
 OS Anemia phyllitidis (Fern).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Filicophyta; Filicopsida; Filicales; Schizaeaceae; Anemia.  
 OX NCBI\_TaxID=12940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vuorek O., Moepes B., Schraudolf H.;  
 RT "cDNA cloning of poly(A)-binding proteins from fern Anemia  
 phyllitidis."  
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY030359; AAK51123.1; -  
 FT NON\_TER 1 1  
 SQ SEQUENCE 472 AA; 51880 MW; 85499785D003B424 CRC64;

Query Match 48.3%; Score 43; DB 10; Length 472;  
 Best Local Similarity 50.0%; Pred. No. 49;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPOLQVMMMP 17  
 DB 318 Q00PMLQ00MPLRG 333

RESULT 13  
 Q9M6E4 PRELIMINARY; PRT; 479 AA.  
 AC Q9M6E4:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE POLY(A)-BINDING PROTEIN (FRAGMENT).  
 GN PABP.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Le H., Gallie D.R.;  
 RT "Sequence diversity and conservation of the poly(A)-binding protein in  
 plants."  
 RL Plant Sci. 152:101-114(2000).  
 DR EMBL; AF190657; AAF66825.1; -  
 DR HSSP; P11940; 1CVJ.  
 DR InterPro: IPR002004; PABP.  
 DR InterPro: IPR000504; RRM.  
 DR Pfam; PF00658; PABP; 1.  
 DR Pfam; PF00076; rrm; 2.  
 DR SMART; SM00517; POLYA; 1.  
 DR SMART; SM00360; RRM; 2.  
 DR PROSITE; PS50102; RRM; 2.  
 DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 479 AA; 52626 MW; A2C3F46C3D688A12 CRC64;

Query Match 48.3%; Score 43; DB 10; Length 479;

Best Local Similarity 53.3%; Pred. No. 50;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPOLQVMMMP 16

DB 324 Q0PMLQ00MPLRG 338

RESULT 14

057224 PRELIMINARY; PRT; 639 AA.  
 AC 057224:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 GN ORF11.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
 OC Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-95207419; PubMed-7899523;  
 RA Flanagan S.E., Zitzow L.A., Su Y.A., Clewell D.B.;  
 RT "Nucleotide sequence of the 18-kb conjugative transposon Tn916 from  
 Enterococcus faecalis."  
 RL Plasmid 32:350-354(1994).  
 RN [2]  
 RP SEQUENCE OF 636-639 FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-94134828; PubMed-8302931;  
 RA Su Y.A., Clewell D.B.;  
 RT "Characterization of the left 4 kb of conjugative transposon Tn916:  
 determinants involved in excision."  
 RL Plasmid 30:234-250(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-92368175; PubMed-133953;  
 RA Su Y.A., He P., Clewell D.B.;  
 RT "Characterization of the tet(M) determinant of Tn916: evidence for  
 regulation by transcription attenuation."  
 RL Antimicrob. Agents Chemother. 36:769-778(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RA Clewell D.B.;  
 RT Submitted (May-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U09422; AAB60022.1; -  
 DR EMBL; M85225; AAA24784.1; -  
 DR HSSP; P13551; IFNM.  
 DR InterPro: IPR000640; EFG\_C.  
 DR InterPro: IPR000795; GTP\_EFTU.  
 DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 DR Pfam; PF00679; EFG\_C; 1.  
 DR Pfam; PF00009; GTP\_EFTU; 1.  
 DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS; PR00315; ELONGATNFC.  
 DR PROSITE; PS00301; EFACOR\_GTP; 1.  
 KW GTP-binding.  
 SQ SEQUENCE 639 AA; 72491 MW; D5299DCA60467C3D CRC64;

Query Match 48.3%; Score 43; DB 2; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 67;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPOLQVMMMP 14  
 DB 339 IENPHPLQTVTEP 352

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RESULT 15
Q9AC90 ID Q9AC90 PRELIMINARY; PRT; 639 AA.
AC Q9AC90;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TET(M).
GN TET(M).
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21220755; Pubmed=11320127;
RA "Roberts A.P., Johannesen P.A., Lytras D., Mullany P., Rood J.I.;
RT "Comparison of Tn3397 from Clostridium difficile, Tn916 from
RT Enterococcus faecalis and the CW459rel(M) element from Clostridium
RT perfringens shows that they have similar conjugation regions but
RT different insertion and excision modules.";
RL Microbiology 147:1243-1251(2001).
DR EMBL: AE329848; AKI7952.1; -.
DR HSSP: P1351; IDAR.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATNFACT.
DR PROSITE: PS00301; EFACITOR_GTP; 1.
KW GTP-binding.
SQ SEQUENCE 639 AA; 72537 MW; 54096C17047F9865 CRC64;

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Query Match 48.3%; Score 43; DB 2; Length 639;
Best local Similarity 50.0%; Pred. No. 67;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 LGTPQPLQVMEP 14
:::|||||:::
DB 339 IENPHILQTTVER 352

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Search completed: July 31, 2002, 15:27:00  
Job time: 213 sec